REMARKS

Reconsideration of the rejections set forth in the Office Action mailed February 26, 2002, is respectfully requested. With entry of this amendment, claims 4-7, 21-23, and 32 have been cancelled; claims 1-3, 8-20, and 24-31 have been amended; and new claims 33-64 have been added. The amendments and new claims are supported in the original specification, e.g., at page 3, line 1 to page 4, line 18; page 5, line 12 to page 7, line 4; page 7, line 26 to page 8, line 6; and page 8, line 23 to page 10, line 14. Therefore, these amendments are made without introducing new matter. As such, claims 1-3, 8-20, 24-31, and 33-64 remain pending in this case.

Applicants have amended the claims to overcome various claim language informalities arising from the European claim style of the originally filed application. The Examiner is encouraged to contact the undersigned at (949) 737-2900 if similar issues arise, so that prosecution of the application may be expedited. The enumerated paragraphs of this section correspond to the numbered remarks in the Examiner's Report.

2. Drawings

Applicants submit formalized drawings herewith for the draftperson's review.

3. Specification

The Examiner has indicated that headings must be inserted for the appropriate sections of the specification, as outlined in the office action (pages 3-4). Appropriate headings for the Title, Background, Summary, Brief Description of the Figures, and Detailed Description of the Invention have been added.

4. Use of Trademark

The Examiner has indicated that, although the use of the trademark LiChrosphere is permitted, it should be capitalized wherever it appears in the specification and be accompanied by the generic technology. Accordingly, Applicants have amended the specification on pages 13 and 14 to include "LiChrosphere® 100 RP-181 column."

35 U.S.C. §112, second paragraph

6. Claims 1-20, 22-24, and 26-32 were rejected under 35 U.S.C. § 112, second paragraph, as being purportedly indefinite for failing to particularly point out and distinctly claim the subject matter that the Applicants regard as the invention.

7. Claim 1 was rejected as being allegedly indefinite for reciting the limitations "the recognition species B" in line 10 and "the form" in line 14 without sufficient antecedent basis for these limitations in the claim. Claim 1 has been amended to claim "a complementary recognition sequence" and "forms a molecular pairing system."

In addition, the recitation of "can bind" in line 11 was objected to for allegedly rendering the claim vague and indefinite because it is unclear whether A and B must bind or not. Applicants have amended claim 1 to note that the complementary recognition sequence binds to the capture sequence. Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

8. Claim 2 was rejected as being allegedly indefinite for reciting the limitation "the pairing system" in lines 16-17 without sufficient antecedent basis. Applicants have amended claim 2 to recite "the molecular pairing system." Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

9. Claim 3 was rejected as allegedly being indefinite for containing improper Markush language. Claim 3 has been amended to claim non-covalent interactions that are "selected from a group consisting of hydrogen bridges, ..." Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

10. Claim 4 was rejected as being allegedly indefinite for reciting the limitation "the molecular pairing system" in lines 25-26 without sufficient antecedent basis. Applicants have cancelled claim 4, thereby mooting this rejection. As such, Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

11. Claim 5 was objected to as being allegedly indefinite for reciting the broad range of "a pentose" and also reciting the narrower range of "a pentopyranose or pentofuranose." Applicants have cancelled claim 5, thereby mooting this rejection. As such, Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

12. Claims 6-9 were rejected as being allegedly indefinite for containing improper Markush language. Claims 6 and 7 have been cancelled, thereby mooting this rejection. Claims 8 and 9 have been amended to include the phrase wherein the moiety is "selected from the group consisting of ...." Applicants respectfully request reconsideration of the amended claims and withdrawal of the rejection.

13. Claim 8 was objected to as being allegedly indefinite for reciting the limitation "the nucleobase" without sufficient antecedent basis. Claim 8 has been amended to recite "at least one nucleobase." Applicants also note that nucleobase moieties are an inherent part of a nucleic acid or nucleic acid analog. Therefore, Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

14. Claim 10 was objected to as being allegedly indefinite for reciting the broad range of a length of 4-50 nucleotides and also reciting a narrower range of lengths of 4-25, 4-15, and 4-10 nucleotides. Applicants have amended the claims, deleting the narrower ranges of lengths from claim 10 and including them in new dependent claims 35-37. Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

15. Claim 12 was rejected as being allegedly indefinite for containing improper Markush language. Applicants have amended claim 12 to include language wherein the moiety is "selected from the group consisting of ...." Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

16. Claim 12 was objected to as being allegedly indefinite for reciting a broad range of carriers and also reciting a narrower range of carriers. Applicants have amended claim 12, deleting the narrower ranges from claim 12 and including them in new dependent claims 38-40. Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

17. Claims 12 and 13 were objected to as being allegedly indefinite due to the phrase "such as." Accordingly, claims 12 and 13 have been amended, deleting these phrases and including them in newly added claims 38-41. Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

18. Claim 13 was objected as being allegedly indefinite for reciting the broad range of molecular species and also reciting a narrower range of molecular species. Applicants have amended the claims, deleting the narrower ranges from claim 13 and including them in new dependent claim 41.

Therefore, Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

19. Claim 14 was objected to as being allegedly indefinite for reciting the broad range of molecular species and also reciting a narrower range of molecular species. Applicants have amended claim 14, deleting the narrower range of "in a matrix" and including it in new dependent claim 43. Therefore, Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

20. Claim 14 was objected to as being allegedly indefinite for reciting the limitation "the form" with insufficient antecedent basis. Applicants have amended claim 14, deleting "preferably in the form of a matrix." New claim 43 has been added without the superfluous "the form of." Therefore, Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

21. Claim 18 were objected to as being allegedly indefinite due to the phrase "such as" and the following lists of specific embodiments. Accordingly, claim 18 has been amended, deleting these phrases. Applicants reserve the right to add dependent claims to these specific embodiments at a later point in time. Therefore, Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

22. Claim 19 was objected as being allegedly indefinite for the recitation of "can bind" for allegedly rendering the claim vague and indefinite because it is unclear whether A and B must bind or not. Applicants have amended the claim to note that various recognition sequences bind to the capture sequence. As a result, Applicants respectfully request reconsideration of the amended claim and withdrawal of the rejection.

23. Claims 22 and 23 were rejected as being allegedly vague and indefinite because the value of n was not defined. Applicants have cancelled claims 22 and 23, thereby mooting this rejection. Applicants respectfully request withdrawal of this rejection.

24. Claim 23 was objected to as being allegedly indefinite for reciting the limitation "the structure" with insufficient antecedent basis. Applicants have cancelled claim 23, thereby mooting this rejection. Applicants respectfully request withdrawal of this rejection.

25. Claim 24 was objected to as being allegedly indefinite for reciting the limitations "the different recognition species B" and "the same substrate S" with insufficient antecedent basis. Applicants have amended claim 24 to recite "the various biomolecules" and "the [same] substrate S," which was introduced in claim 4 from which this claim indirectly depends. Applicants respectfully request reconsideration of the amended claim and withdrawal of the objection.

26a. Claim 26 has been amended for clarification.

26. Claim 27 was objected to as being allegedly indefinite for reciting the limitations "the identification", "the aid", and "the formation" with insufficient antecedent basis. Claim 27 was also objected to as being allegedly vague because it was unclear what was brought into contact with B. Applicants have reworded claim 27 to put it in the active tense. In addition, claim 27 no longer refers to "the recognition system according to claim 1." The phrase "with the aid of" has also been deleted. Applicants believe that these amendments take care of the above objections and respectfully requests withdrawal of the objection and reconsideration of the amended claim.

27. Claims 28 and 29 were objected to for purportedly being indefinite due to the phrase "such as." Accordingly, claims 28 and 29 have been amended, deleting these phrases and including them in newly added claims 44 and 45. Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

28. Claim 29 was objected to for purportedly being indefinite due to the phrase "for example" since it is unclear whether the limitation following the phrase is part of the claimed invention. Applicants have deleted this phrase from claim 29 and included the subject matter in new claim 45. Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

29. Claim 29 was objected to as being allegedly indefinite for reciting the limitations "the environment" and "the electrode" with insufficient antecedent basis. Accordingly, newly added claim 45 includes "an environment" and "an electrode." Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

30. Claim 31 was objected to as being allegedly indefinite for reciting the limitation "the binding equilibrium" with insufficient antecedent basis. Accordingly, claim 31 has been amended to recite the limitation "a binding equilibrium." Therefore, Applicants respectfully request reconsideration of the amended claims and withdrawal of the objection.

31-33. Applicants note that claim 32 has been cancelled, and thus, the rejections directed towards claim 32 in paragraphs 31-33 are moot. Applicants respectfully request withdrawal of these rejections.

CONCLUSION

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

Applicants submit that the claims, as amended, are free of the cited art and are in position for allowance. If the Examiner has any questions regarding this communication, or feels that an interview might facilitate prosecution of the application, he is invited to contact the undersigned at (949) 737-2900.

Respectfully submitted,

O'MELVENY & MYERS LLP

Dated: 11/5/02

By: John Kappos

John Kappos
Reg. No. 37,861

400 South Hope Street
Los Angeles, California 90071-2899
(213) 430-6000

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

On page 1, line 8, please insert the following:

-- This is the U.S. national application of PCT Application No. EP98/06001, filed on Sept. 21, 1998, which claims priority from German Application No. 197 41 716.7, filed on Sept. 22, 1997. --

On page 1, line 9, please insert the following heading:

-- Field of the Invention --

On page 1, line 16, please insert the following heading:

-- Background --

On page 10, line 19, please replace the heading with the following:

-- Brief Description of the Figures --

On page 11, line 26, please insert the following:

-- Detailed Description of the Invention

This invention is described by the several following examples. --

On page 13, lines 22-23, please replace with the following:

-- Column material: 10 µM LiChrosphere® 100 RP-18 column from Merck Darmstadt GmbH; 250 x 4 mm --

On page 14, lines 32-33, please replace with the following:

-- Column material: 10 µM Lichrosphere® 100 RP-18 column from Merck Darmstadt GmbH; 250 x4 --

Please replace page 14, line 36 with the following:

-- Mass spectrometry: calculated mass MH_2^{2+}: 1436.2 g/mol

found mass MH_2^{2+}: 1436.4 g/mol --

Please delete lines 5-6 on page 15.

Please replace the text on page 17, lines 5 with the following:

-- What is claimed is: --

In the Claims

Please cancel claims 4-7, 21-23, and 32.

Please amend claims 1-3, 8-20, and 24-31 as follows.

Please add new claims 33-64.

1. (Amended) A r[R]ecognition system comprising:

(a) at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units [binding component A having at least one binding site for the recognition species B]; and

(b) at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, [recognition species B which can bind to the binding component A and contains at least one binding site for a substrate S, characterized in that] and wherein the binding of the capture sequence to the recognition sequence forms [binding component A to the recognition species B takes place in the form of] a molecular pairing system.

2. (Amended) The r[R]ecognition system according to c[C]laim 1, wherein the molecular [characterized in that the] pairing system is a complex that [which] is formed by association of the capture sequence with the complementary recognition sequence [binding component A with the recognition species B] via non-covalent interactions.

3. (Amended) The r[R]ecognition system according to c[C]laim 2, wherein [characterized in that] the non-covalent interactions are selected from the group consisting of hydrogen bridges, salt bridges, stacking, metal ligands, charge-transfer complexes, and hydrophobic interactions.

8. (Amended) The r[R]ecognition system according to claim 1[4], wherein at least one [characterized in that the] nucleobase of the capture or recognition sequences [nucleic acid or its analogues] is selected from the group consisting of purine, 2,6-diaminopurine, 6-purinethiol, pyridine, pyrimidine, adenine, guanine, isoguanine, 6-thioguanine, xanthine, hypoxanthine, thymine[thymidine], cytosine, isocytosine, indole, tryptamine, N-phthaloyltryptamine, uracil, caffeine, theobromine, theophylline, benzotriazole, and [or] acridine.

9. (Amended) The r[R]ecognition system according to claim 1[4], wherein the p-NA is [characterized in that the nucleic acid analogues are] selected from the group consisting of ribopyranosyladenosine, ribopyranosylguanosine, ribopyranosylthymidine, ribopyranosylcytosine, ribopyranosyltryptamine or ribopyranosyl-N-phthalotryptamine, ribopyranosyluracil, and [or] their 2-amino-4-(carboxymethyl)ribopyranosyl[]] derivatives.

10. (Amended) The r[R]ecognition system according to claim 1[4], wherein the length of the capture or recognition sequences are [characterized in that the length of the nucleic acid and its analogues is] at least about 4-50 [, preferably at least about 4-25, in particular at least about 4-15, especially at least about 4-10,] nucleotides.

11. (Amended) The r[R]ecognition system according to claim 1, wherein the capture sequence [characterized in that the binding component A] is immobilized on a carrier.

12. (Amended) The r[R]ecognition system according to c[C]laim 11, wherein [characterized in that] the carrier is selected from the group consisting of ceramic, metal, [in particular noble metal,] glasses, polymers[plastics], and crystalline materials. [or thin layers of the carrier, in particular of the materials mentioned, or (bio)molecular filaments, such as cellulose, structural proteins.]

13. (Amended) The r[R]ecognition system according to c[C]laim 11, wherein the capture sequence [characterized in that the binding component A] is immobilized on the [a] carrier by means of a covalent bond, quasi-covalent bond or supramolecular bond by association of two or more molecular species [such as molecules of linear constitution, in particular peptides, peptoids, proteins, linear oligo- or polysaccharides, nucleic acids and their analogues, or monomers such as

heterocycles, in particular nitrogen heterocycles, or molecules of non-linear constitution such as branched oligo- or polysaccharides or antibodies and their functional moieties such as Fv fragments, single-chain Fv fragments (scFv) or Fab fragments].

14. (Amended) The r[R]ecognition system according to claim 11, wherein the capture sequence [characterized in that the binding component A] is immobilized at defined sites of the carrier[, preferably in the form of a matrix].

15. (Amended) The r[R]ecognition system according to c[C]laim 14, wherein [characterized in that] the defined sites of the carrier are addressed.

16. (Amended) The r[R]ecognition system according to claim 11, wherein the capture sequence [characterized in that the binding component A] is immobilized on a carrier electrode of the carrier.

17. (Amended) The r[R]ecognition system according to claim 1, wherein the binding site is a biomolecule that binds substrate S. [characterized in that the recognition species B is a biomolecule.]

18. (Amended) The r[R]ecognition system according to c[C]laim 17, wherein [characterized in that] the biomolecule is selected from the group consisting of peptides, peptoids, proteins, [such as receptor or functional moieties thereof such as the extracellular domain of a membrane receptor, antibodies or functional moieties thereof such as Fv fragments, single-chain Fv fragments (scFv) or Fab fragments, or cell constituents such as] lipids, glycoproteins, filament constituents, [or] viruses, [viral constituents such as capsids, or] viroids, [or their derivatives such as acetates and their active moieties, or substance libraries such as ensembles of structurally differing compounds, preferably oligomeric or polymeric peptides, peptoids,] saccharides, nucleic acids, and their active moieties.

19. (Amended) The r[R]ecognition system according to claim 1[4], wherein the immobilized capture sequence [characterized in that the immobilized binding component A] contains various binding sites for the complementary recognition sequence, by means of which

various complementary recognition sequences bind to the capture sequence. [various recognition species B, by means of which various recognition species B 15 can bind to the binding component A.]

20. (Amended) The r[R]ecognition system according to claim 1[4], wherein [characterized in that] at least one further complementary recognition sequence is bound to [recognition species B is immobilized on] the capture sequence. [binding component A.]

24. (Amended) The r[R]ecognition system according to claim 34[19], wherein [characterized in that] the various biomolecules bind the [different recognition species B recognize the same] substrate S.

25. (Amended) The r[R]ecognition system according to c[C]laim 24, wherein the substrate S is selected from the group consisting of peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, saccharides, nucleic acids, and their active moieties. [characterized in that the substrate S is selected from molecules, preferably pharmaceuticals and plant protection active compounds, metabolites, physiological messenger substances, derivatives of lead structures, substances which are produced or produced to an increased extent in the human or animal body in the case of pathological changes, or transition state analogues, or peptides, peptoids, proteins such as receptors or functional moieties thereof such as the extracellular domain of a membrane receptor, antibodies or functional moieties thereof such as Fv fragments, single-chain Fv fragments (scFv) or Fab fragments, or cell constituents such as lipids, glycoproteins, filament constituents, or viruses, viral constituents such as capsids, or viroids, or their derivatives such as acetates, or monomers such as heterocycles, in particular nitrogen heterocycles, or molecules of non-linear constitution such as branched oligo- or polysaccharides, or substance libraries such as ensembles of structurally differing compounds, preferably oligomeric or polymeric peptides, peptoids, saccharides, nucleic acids, esters, acetals or monomers such as heterocycles, lipids, steroids, or structures in which pharmaceuticals act, preferably pharmaceutical receptors, voltage-dependent ion channels, transporters, enzymes or biosynthesis units of microorganisms.]

26. (Amended) The r[R]ecognition system according to claim 1, wherein the at least one binding site for substrate S comprises antibodies, antibody fragments, and derivatives thereof. [characterized in that it is an immunoassay.]

27. (Amended) A p[P]rocess for identifying [the identification of] a substrate S in a sample, [with the aid of the recognition system according to claim 1, characterized in that] the process comprising:

(a) providing a recognition system comprising:

at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, and wherein the binding of the capture sequence to the recognition sequence forms a molecular pairing system;

(b[a]) contacting the recognition sequence containing at least one binding site for substrate S with a sample containing substrate S;[a recognition species B which recognizes the substrate S is brought into contact with the sample,]

(c[b]) simultaneously or successively contacting the recognition sequence and sample with the immobilized capture sequence to form an immobilized complex; and[is simultaneously or successively brought into contact with an immobilized recognition species B, and]

(d[c]) detecting a complex of immobilized capture sequence, recognition sequence, and substrate S. [the formation of a complex of immobilized binding component A, recognition species B and substrate S is detected.]

28. (Amended) The p[P]rocess according to c[C]laim 27, wherein [characterized in that] the formation of the complex is controlled by means of physical parameters [such as temperature, salts, solvents, electrophoretic processes].

29. (Amended) The p[P]rocess according to c[C]laim 27[8], wherein [characterized in that] the complex is detected by means of a label on the complex [labelling such as radioactive or fluorescent labelling, enzymatic labelling, redox labelling, spin labelling of the recognition species B,] or by directly detecting [means of] the complex itself[, for example by means of electrode processes such as by means of chemical processes, e.g. redox processes in the environment or on the electrode or by means of a physical parameter such as by means of impedance measurement or direct current measurement].

30. (Amended) The p[P]rocess according to claim 27, further comprising isolating [characterized in that] the complex of the recognition sequence [species B] and substrate S [is isolated in a further step].

31. (Amended) The p[P]rocess according to c[C]laim 27[30], wherein [characterized in that] the complex of recognition sequence [species B] and substrate S is in a binding equilibrium, and further comprising isolating the complex [isolated] after freezing the binding equilibrium [or covalent cross-linking of recognition species B and substrate S].

33. (New) The process according to claim 30, further comprising the step of covalently cross-linking the recognition sequence and substrate S.

34. (New) The recognition system according to claim 20, wherein the binding site of at least one further complementary recognition sequence is an additional biomolecule.

35. (New) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-25 nucleotides.

36. (New) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-15 nucleotides.

37. (New) The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-10 nucleotides.

38. (New) The recognition system according to Claim 11, wherein the carrier comprises a noble metal.

39. (New) The recognition system according to Claim 11, wherein the carrier comprises a (bio)molecule polymer.

40. (New) The recognition system according to Claim 11, wherein the carrier comprises a structural protein.

41. (New) The recognition system according to Claim 13, wherein the two or more molecular species are selected from a group consisting of peptides, peptoids, proteins, linear oligo- or polysaccharides, nucleic acids, heterocycles, branched oligo- or polysaccharides, antibodies, and derivatives thereof.

42. (New) The recognition system according to Claim 1, wherein the p-NA is a pyranosyl-RNA (p-RNA).

43. (New) The recognition system according to claim 11, wherein the capture sequence is immobilized at defined sites of the carrier in a matrix.

44. (New) The process of claim 28, wherein the physical parameters are selected from the group consisting of temperature, salts, solvents, and electrophoretic processes.

45. (New) The process according to Claim 29, wherein the complex is detected by means of radioactive labeling, fluorescent labeling, enzymatic labeling, redox labeling, spin labeling of the

recognition sequence, redox processes in an environment or on an electrode, impedance measurement, or direct current measurement.

46. (New) A recognition system comprising:

at least one immobilized capture sequence that is synthetic and does not bind to naturally occurring nucleic acids; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is synthetic and does not bind to naturally occurring nucleic acids, wherein the binding of the recognition sequence to the capture sequence forms a non-covalent, hydrogen-bonded molecular pairing system.

47. (New) The recognition sequence of claim 46, wherein the capture and/or recognition sequences are selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units.

48. (New) The recognition sequence of claim 47, wherein the p-NA is a pyranosyl RNA (p-RNA).

49. (New) The recognition sequence of claim 46, wherein the binding site is a biomolecule that binds substrate S.

50. (New) The recognition sequence of claim 49, wherein the biomolecule is selected from peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, antibodies, antibody fragments, saccharides, and nucleic acids, and their active moieties,

51. (New) The recognition system according to claim 47, wherein the p-NA is selected from the group consisting of ribopyranosyladenosine, ribopyranosylguanosine, ribopyranosylthymidine, ribopyranosylcytosine, ribopyranosyltryptamine or ribopyranosyl-N-phthalotryptamine, ribopyranosyluracil, and their 2-amino-4-(carboxymethyl)ribopyranosyl derivatives.

52. (New) The recognition system according to claim 46, wherein the capture sequence is immobilized on a carrier.

53. (New) The recognition system according to claim 52, wherein the capture sequence is immobilized at defined sites of the carrier.

54. (New) The recognition system according to claim 52, wherein the capture sequence is immobilized on a carrier electrode of the carrier.

55. (New) The recognition system according to claim 46, wherein the immobilized capture sequence contains various binding sites for the complementary recognition sequence, by means of which various complementary recognition sequences binds to the capture sequence.

56. (New) The recognition system according to claim 55, wherein at least one further complementary recognition sequence is bound to the capture sequence, wherein the binding site of at least one further complementary recognition sequence is an additional biomolecule that binds the substrate S.

57. (New) A process for identifying a substrate S in a sample, the process comprising:

(a) providing a recognition system comprising:

at least one immobilized capture sequence that is synthetic and does not bind to naturally occurring nucleic acids; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is synthetic and does not bind to naturally occurring nucleic acids, wherein the binding of the recognition sequence to the capture sequence forms a non-covalent, hydrogen-bonded molecular pairing system.

(b) contacting the recognition sequence containing at least one binding site for substrate S with a sample containing substrate S;

(c) simultaneously or successively contacting the recognition sequence and sample with the immobilized capture sequence to form an immobilized complex; and

(d) detecting a complex of immobilized capture sequence, recognition sequence, and substrate S.

58. (New) The process according to claim 57, wherein the formation of the complex is controlled by means of physical parameters.

59. (New) The process according to claim 58, wherein the physical parameters are selected from the group consisting of temperature, salts, solvents, and electrophoretic processes.

60. (New) The process according to claim 57, wherein the complex is detected by means of a label on the complex or by directly detecting the complex itself.

61. (New) The process according to claim 60, wherein the complex is detected by means of radioactive labeling, fluorescent labeling, enzymatic labeling, redox labeling, spin labeling of the recognition sequence, redox processes in an environment or on an electrode, impedance measurement, or direct current measurement.

62. (New) The process according to claim 57, further comprising isolating the complex of the recognition sequence and substrate S.

63. (New) The process according to claim 57, wherein the complex of the recognition sequence and substrate S is in a binding equilibrium, and further comprising isolating the complex after freezing the binding equilibrium.

64. (New) The process according to claim 62, further comprising the step of covalently cross-linking the recognition sequence and substrate S.

FEES FOR CLAIMS:

☐ Applicant claims small entity status pursuant to 37 CFR 1.27.

The fees for claims (37 CFR § 1.16(b)-(d)) have been calculated as shown below:

Total Claims	54	-	54	=	0	x $18.00	0
Independent Claims	4	-	4	=	0	x $84.00	0
Multiple Dependent Claims	$280	(if applicable)				☐	0
TOTAL OF ABOVE CALCULATIONS							0
Reduction by ½ for Filing by Small Entity. Note 37 CFR §§ 1.9, 1.27, 1.28.						☐	0
TOTAL FEES FOR CLAIMS SUBMITTED HEREWITH							0

☒ A check in the amount of **$400.00** is enclosed to cover the above extension fee.

☐ Charge O'Melveny & Myers' Deposit Account No. **500639** in the amount of $___ for the extra claim fees noted above.

☒ The Commissioner is authorized to charge O'Melveny & Myers' Deposit Account No. **500639** for any fees required under 37 CFR §§ 1.16 and 1.17 that are not covered, in whole or in part, by a check enclosed herewith and to credit any overpayments to said Deposit Account **500639.**

Respectfully submitted,

O'MELVENY & MYERS LLP

Dated: 11/5/02

By: John Kappos
John C. Kappos
Reg. No. 37,861

JCK/DKW/dnd

34263
PATENT TRADEMARK OFFICE

O'Melveny & Myers LLP
114 Pacifica, Suite 100
Irvine, CA 92618-3315
(949) 737-2900